AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listing of the claims in the application:

LISTING OF THE CLAIMS:

Claims 1-14 (canceled).

Claim 15. (currently amended) A method for constructing a normalized cDNA library, comprising:

(a) constructing a non-normalized cDNA library from an RNA sample, wherein said RNA sample contains different species of RNA of different amounts, wherein each member of said non-normalized cDNA library is separate from other members;

(b) identifying the relative amounts of each member of said non-normalized cDNA library represented in said RNA sample;

(c) dividing the members of said non-normalized cDNA library into groups; wherein one group of members of said non-normalized cDNA library is represented in low amounts by said RNA sample and one or more groups of members of said non-normalized cDNA library is represented in high amounts by said RNA sample;

(d) selecting a first sub-group of said one or more groups of members of said non-normalized cDNA library represented in high amounts by said RNA sample;

(e) identifying the members in said group of members of said non-normalized cDNA library represented in high amounts by said RNA sample, which is

are not represented within said first sub-group of members selected from said group of members;

(f) forming a second sub-group of members from the members identified in step (e) and repeating step (e) until every member of said group of members of said non-normalized cDNA library represented in high amounts by said RNA sample has been selected within a sub-group of members;

(g) pooling the members of said group of members of said non-normalized cDNA library represented in low amounts by said RNA sample and the members of every sub-group selected in a collection;

whereby said collection is said normalized cDNA library.

Claim 16. (previously presented) The method according to Claim 15, wherein said RNA sample is obtained from a cell.

Claim 17. (previously presented) The method according to Claim 16, wherein said RNA sample is a mRNA sample.

Claim 18. (previously presented) The method according to Claim 16, wherein said cell is a eubacteria, archaebacteria, or eukaryotic cell.

Claim 19. (previously presented) The method according to Claim 18, wherein said eukaryotic cell is a plant cell or animal cell.

Claim 20. (previously presented) The method according to Claim 19, wherein said plant cell is a soy, tobacco, wheat, rice, or corn cell.

Claim 21. (previously presented) The method according to Claim 19, wherein said animal cell is a human, ape, mouse, rat, cow, pig, horse, goat, sheep, dog, cat, chicken, zebrafish, or fruitfly cell.

Claim 22. (previously presented) The method according to Claim 21, wherein said human cell is a human kidney cell.

Claim 23. (previously presented) The method according to Claim 15, wherein said normalized cDNA library is a normalized full-length cDNA library.

Claim 24. (previously presented) The method according to Claim 15, wherein said constructing a non-normalized cDNA library from an RNA sample comprises catalyzing a reverse transcription reaction for each species of said RNA sample, wherein said catalyzing takes place under conditions permissible for catalyzing a reverse transcription reaction.

Claim 25. (previously presented) The method according to Claim 24, wherein said catalyzing comprises:

(i) hybridizing poly-T oligonucleotide primers to said RNA sample;

(ii) adding dATP, dCTP, dGTP, dTTP, and reverse transcriptase; and

(iii) incubating said RNA sample at a temperature permissible for catalyzing a reverse transcription reaction.

Claim 26. (previously presented) The method according to Claim 15, wherein said non-normalized cDNA library is a non-normalized full-length cDNA library.

Claim 27. (previously presented) The method according to Claim 15, further comprising:

transforming each member of said non-normalized cDNA library into a host cell, wherein said transforming step is subsequent to said constructing and prior to said identifying of step (b).

Claim 28. (previously presented) The method according to Claim 27, further comprising:

amplifying each member of said non-normalized cDNA library,

wherein said amplifying comprises growing each said host cell containing cDNA, wherein said amplifying step is subsequent to said transforming and prior to said identifying of step (b).

Claim 29. (previously presented) The method according to Claim 15, wherein said identifying of step (b) comprises:

(i) constructing a labeled probe library from said RNA sample;

(ii) hybridizing said labeled probe library to said non-normalized cDNA library;

(iii) identifying the relative amounts of labeled probe hybridized to each member of said non-normalized cDNA library.

Claim 30. (previously presented) The method according to Claim 15, wherein said identifying of step (e) comprises:

(i) constructing a labeled probe library from said sub-group of members;

(ii) hybridizing said labeled probe library to said group of members;

(iii) identifying each member of said group of members that is not hybridized to by said labeled probe library.

Claim 31. (previously presented) The method according to Claim 15, further comprising:

sequencing a member of said group members of said non-normalized cDNA library represented in low amounts by said RNA sample and a member of every sub-group selected prior to said pooling, wherein a sufficient number of nucleotides are sequenced to identify members that are represented no more than once; and

pooling unique members determined by said sequencing.

Claim 32-42 (canceled).

Claim 43. (previously presented) The method according to claim 15, further comprising repeating steps (d)-(f) with every sub-group of said one or more groups of members of said non-normalized cDNA library represented in high amounts by said RNA sample before step (g);

Claim 44. (previously presented) The method according to claim 31, wherein every member of said group members of said non-normalized cDNA library represented in low amounts by said RNA sample and every member of every sub-group are at least partially sequenced.

Claim 45. (previously presented) The method of claim 44, wherein every unique member is pooled.

Claim 46. (canceled).

Claim 47. (previously presented) The method of claim 15 wherein the one group of members of said non-normalized cDNA library represented in low amounts by said RNA sample constitutes about 30% of all cDNA clones in said non-normalized cDNA library.

Claim 48. (previously presented) The method of claim 15 wherein the RNA sample is from a plurality of different tissues, developmental stages or individuals from the same species of organism.

Claim 49. (previously presented) The method of claim 48 wherein the RNA is from a plurality of different cell types and/or tissue.

Claim 50. (previously presented) The method of claim 49 wherein the RNA is from substantially every cell type and/or tissue from the same species of organism is used.

Claim 51. (previously presented) The method of claim 48 wherein the RNA is from a plurality of different individuals from the same species of organism.

Claim 52. (new) The method of claim 48 wherein the RNA is from a plurality of different tissues, different developmental stages and different individuals from the same species of organism.

Claim 53. (new) The method of claim 52 wherein the RNA further originates from both a normal tissue from a normal individual and a diseased tissue from an individual with a disease.